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Supplemental Material

Genome-Wide Association Study of Susceptibility to Particulate Matter-Associated QT Prolongation

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Table S2. Sensitivity of the PM₁₀ x SNP interaction

Figure S1. Quantile-Quantile (QQ) plot of observed versus expected $-\log_{10} P$ -values of each SNP from the trans-ethnic, fixed-effects meta-analysis of the SNP x PM₁₀ interactions. Lambda is the genomic inflation factor.

Figure S2. A) Predicted mean (95% confidence interval) QT (ms) per unit increase in the coded allele (T) dosage of rs1619661 at PM₁₀ concentrations dichotomized at \leq and $>$ the 50th – 90th percentiles (P50, P60, P70, P80, P90) and the 1987-2006 National Ambient Air Quality Standard (NAAQS*) for annual PM₁₀ (50 $\mu\text{g}/\text{m}^3$), while adjusting for age, geographic region or center, season, calendar year, RR interval, and ancestry. B) Distribution of observed ambient PM₁₀ concentrations labelled with the PM₁₀ dichotomizations.

Figure S3. UCSC Genome Browser displaying rs1619661 (highlighted), associated SNPs (linkage disequilibrium ≥ 0.8), and tracks representing DNase1 hypersensitivity and DNA methylation in cardiac tissues.

Supplemental Material References